RAW SEQUENCE LISTING

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Application Serial Number: _____ 10/516,342
Source: _____ PCT
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RAW SEQUENCE LISTING   DATE: 01/10/2006
PATENT APPLICATION: US/10/516,342   TIME: 08:40:50

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\01102006\J516342.raw**

      5 <110> APPLICANT: Memorial Sloan-Kettering Cancer Center
      7   Kolesnick, Richard N.
      9   Xing, Hong-Mei R.
     13 <120> TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS
MEDIATED
     14   TUMORIGENESIS
     18 <130> FILE REFERENCE: 1216-1-006PCT
W--> 19 US
     22 <140> CURRENT APPLICATION NUMBER: 10/516,342
     23 <141> CURRENT FILING DATE: 2004-11-30
     25 <150> PRIOR APPLICATION NUMBER: PCT/US03/16961
     26 <151> PRIOR FILING DATE: 2003-05-29
     29 <150> PRIOR APPLICATION NUMBER: 60/384,228
     31 <151> PRIOR FILING DATE: 2002-05-30
     35 <150> PRIOR APPLICATION NUMBER: 60/460,023
     37 <151> PRIOR FILING DATE: 2003-04-03
     41 <160> NUMBER OF SEQ ID NOS: 23
     45 <170> SOFTWARE: PatentIn version 3.1
     49 <210> SEQ ID NO: 1
     51 <211> LENGTH: 120
     53 <212> TYPE: DNA
     55 <213> ORGANISM: Homo sapiens
     59 <400> SEQUENCE: 1
     60 ctgcagaagc tcatcgatat ctccatcggc agtctgcgcg ggctgcgcac caagtgctca   60
     62 gtgtctaacg acctcacaca gcaggagatc cggaccctag aggcaaagct ggtgaaatac   120
     65 <210> SEQ ID NO: 2
     67 <211> LENGTH: 41
     69 <212> TYPE: PRT
     71 <213> ORGANISM: Homo sapiens
     75 <400> SEQUENCE: 2
     77 Leu Gln Lys Leu Ile Asp Ile Ser Ile Gly Ser Leu Arg Gly Leu Arg
     78 1   5   10   15
     81 Thr Lys Cys Ser Val Ser Asn Asp Leu Thr Gln Gln Glu Ile Arg Thr
     82   20   25   30
     85 Leu Glu Ala Lys Leu Val Lys Tyr Ile
     86   35   40
     89 <210> SEQ ID NO: 3
     91 <211> LENGTH: 19
     93 <212> TYPE: DNA
     95 <213> ORGANISM: Homo sapiens
     99 <400> SEQUENCE: 3
    100 ggcagtctgc gcgggctgc   19
    103 <210> SEQ ID NO: 4
    105 <211> LENGTH: 18

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109 <213> ORGANISM: Homo sapiens
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114 tcagtgtcta acgacctc                                          18
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119 <211> LENGTH: 18
121 <212> TYPE: DNA
123 <213> ORGANISM: Homo sapiens
127 <400> SEQUENCE: 5
128 cggaccctag aggcaaag                                          18
131 <210> SEQ ID NO: 6
133 <211> LENGTH: 19
135 <212> TYPE: DNA
137 <213> ORGANISM: Artificial Sequence
141 <220> FEATURE:
143 <223> OTHER INFORMATION: antisense oligonucleotide
145 <400> SEQUENCE: 6
146 cagcccgcgc agactgccg                                         19
149 <210> SEQ ID NO: 7
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153 <212> TYPE: DNA
155 <213> ORGANISM: Artificial Sequence
159 <220> FEATURE:
161 <223> OTHER INFORMATION: antisense oligonucleotide
163 <400> SEQUENCE: 7
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169 <211> LENGTH: 16
171 <212> TYPE: DNA
173 <213> ORGANISM: Artificial Sequence
177 <220> FEATURE:
179 <223> OTHER INFORMATION: antisense oligonucleotide
181 <400> SEQUENCE: 8
182 ctttgcctct agggtc                                            16
185 <210> SEQ ID NO: 9
187 <211> LENGTH: 873
189 <212> TYPE: PRT
191 <213> ORGANISM: Mus musculus
195 <400> SEQUENCE: 9
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198 1               5                   10                  15
201 Gly Gly Gly Gly Gly Ala Ala Ala Asp Gly Gly Ala Gly Ala Ala Val
202             20                  25                  30
205 Ser Arg Ala Leu Gln Gln Cys Gly Gln Leu Gln Lys Leu Ile Asp Ile
206         35                  40                  45
209 Ser Ile Gly Ser Leu Arg Gly Leu Arg Thr Lys Cys Ser Val Ser Asn
210     50                  55                  60
213 Asp Leu Thr Gln Gln Glu Ile Arg Thr Leu Glu Ala Lys Leu Val Lys
214 65                  70                  75                  80
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217 Tyr Ile Cys Lys Gln Gln Gln Ser Lys Leu Ser Val Thr Pro Ser Asp
218             85                  90                  95
221 Arg Thr Ala Glu Leu Asn Ser Tyr Pro Arg Phe Ser Asp Trp Leu Tyr
222             100                 105                 110
225 Ile Phe Asn Val Arg Pro Glu Val Val Gln Glu Ile Pro Gln Glu Leu
226             115                 120                 125
229 Thr Leu Asp Ala Leu Leu Glu Met Asp Glu Ala Lys Ala Lys Glu Met
230     130             135                 140
233 Leu Arg Arg Trp Gly Ala Ser Thr Glu Glu Cys Ser Arg Leu Gln Gln
234 145             150                 155                 160
237 Ala Leu Thr Cys Leu Arg Lys Val Thr Gly Leu Gly Gly Glu His Lys
238             165                 170                 175
241 Met Asp Ser Gly Trp Ser Ser Thr Asp Ala Arg Asp Ser Ser Leu Gly
242             180                 185                 190
245 Pro Pro Met Asp Met Leu Ser Ser Leu Gly Arg Ala Gly Ala Ser Thr
246             195                 200                 205
249 Gln Gly Pro Arg Ser Ile Ser Val Ser Ala Leu Pro Ala Ser Asp Ser
250     210             215                 220
253 Pro Val Pro Gly Leu Ser Glu Gly Leu Ser Asp Ser Cys Ile Pro Leu
254 225             230                 235                 240
257 His Thr Ser Gly Arg Leu Thr Pro Arg Ala Leu His Ser Phe Ile Thr
258             245                 250                 255
261 Pro Pro Thr Thr Pro Gln Leu Arg Arg His Ala Lys Leu Lys Pro Pro
262             260                 265                 270
265 Arg Thr Pro Pro Pro Pro Ser Arg Lys Val Phe Gln Leu Leu Pro Ser
266             275                 280                 285
269 Phe Pro Thr Leu Thr Arg Ser Lys Ser His Glu Ser Gln Leu Gly Asn
270     290             295                 300
273 Arg Ile Asp Asp Val Thr Pro Met Lys Phe Glu Leu Pro His Gly Ser
274 305             310                 315                 320
277 Pro Gln Leu Val Arg Arg Asp Ile Gly Leu Ser Val Thr His Arg Phe
278             325                 330                 335
281 Ser Thr Lys Ser Trp Leu Ser Gln Val Cys Asn Val Cys Gln Lys Ser
282             340                 345                 350
285 Met Ile Phe Gly Val Lys Cys Lys His Cys Arg Leu Lys Cys His Asn
286             355                 360                 365
289 Lys Cys Thr Lys Glu Ala Pro Ala Cys Arg Ile Thr Phe Leu Pro Leu
290     370             375                 380
293 Ala Arg Leu Arg Arg Thr Glu Ser Val Pro Ser Asp Ile Asn Asn Pro
294 385             390                 395                 400
297 Val Asp Arg Ala Ala Glu Pro His Phe Gly Thr Leu Pro Lys Ala Leu
298             405                 410                 415
301 Thr Lys Lys Glu His Pro Pro Ala Met Asn Leu Asp Ser Ser Ser Asn
302             420                 425                 430
305 Pro Ser Ser Thr Thr Ser Ser Thr Pro Ser Ser Pro Ala Pro Phe Leu
306             435                 440                 445
309 Thr Ser Ser Asn Pro Ser Ser Ala Thr Thr Pro Pro Asn Pro Ser Pro
310             450                 455                 460
313 Gly Gln Arg Asp Ser Arg Phe Ser Phe Pro Asp Ile Ser Ala Cys Ser
```

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314 465                    470                 475                    480
317 Gln Ala Ala Pro Leu Ser Ser Thr Ala Asp Ser Thr Arg Leu Asp Asp
318                475                     490                    495
321 Gln Pro Lys Thr Asp Val Leu Gly Val His Glu Ala Glu Ala Glu Glu
322                500                     505                    510
325 Pro Glu Ala Gly Lys Ser Glu Ala Glu Asp Asp Glu Glu Asp Glu Val
326         515                    520                    525
329 Asp Asp Leu Pro Ser Ser Arg Arg Pro Trp Arg Gly Pro Ile Ser Arg
330     530                    535                    540
333 Lys Ala Ser Gln Thr Ser Val Tyr Leu Gln Glu Trp Asp Ile Pro Phe
334 545                    550                    555                    560
337 Glu Gln Val Glu Leu Gly Glu Pro Ile Gly Gln Gly Arg Trp Gly Arg
338                565                    570                    575
341 Val His Arg Gly Arg Trp His Gly Glu Val Ala Ile Arg Leu Leu Glu
342                580                    585                    590
345 Met Asp Gly His Asn Gln Asp His Leu Lys Leu Phe Lys Lys Glu Val
346         595                    600                    605
349 Met Asn Tyr Arg Gln Thr Arg His Glu Asn Val Val Leu Phe Met Gly
350     610                    615                    620
353 Ala Cys Met Asn Pro Pro His Leu Ala Ile Ile Thr Ser Phe Cys Lys
354 625                    630                    635                    640
357 Gly Arg Thr Leu His Ser Phe Val Arg Asp Pro Lys Thr Ser Leu Asp
358                645                    650                    655
361 Ile Asn Lys Thr Arg Gln Ile Ala Gln Glu Ile Ile Lys Gly Met Gly
362                660                    665                    670
365 Tyr Leu His Ala Lys Gly Ile Val His Lys Asp Leu Lys Ser Lys Asn
366         675                    680                    685
369 Val Phe Tyr Asp Asn Gly Lys Val Val Ile Thr Asp Phe Gly Leu Phe
370     690                    695                    700
373 Gly Ile Ser Gly Val Val Arg Glu Glu Arg Arg Glu Asn Gln Leu Lys
374 705                    710                    715                    720
377 Leu Ser His Asp Trp Leu Cys Tyr Leu Ala Pro Glu Ile Val Arg Glu
378                725                    730                    735
381 Met Ile Pro Gly Arg Asp Glu Asp Gln Leu Pro Phe Ser Lys Ala Ala
382         740                    745                    750
385 Asp Val Tyr Ala Phe Gly Thr Val Trp Tyr Glu Leu Gln Ala Arg Asp
386         755                    760                    765
389 Trp Pro Phe Lys His Gln Pro Ala Glu Ala Leu Ile Trp Gln Ile Gly
390     770         ᵇ             775                    780
393 Ser Gly Glu Gly Val Arg Arg Val Leu Ala Ser Val Ser Leu Gly Lys
394 785                    790                    795                    800
397 Glu Val Gly Glu Ile Leu Ser Ala Cys Trp Ala Phe Asp Leu Gln Glu
398                805                    810                    815
401 Arg Pro Ser Phe Ser Leu Leu Met Asp Met Leu Glu Arg Leu Pro Lys
402         820                    825                    830
405 Leu Asn Arg Arg Leu Ser His Pro Gly His Phe Trp Lys Ser Ala Asp
406         835                    840                    845
409 Ile Asn Ser Ser Lys Val Met Pro Arg Phe Glu Arg Phe Gly Leu Gly
410     850                    855                    860
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413 Thr Leu Glu Ser Gly Asn Pro Lys Met
414 865                 870
417 <210> SEQ ID NO: 10
419 <211> LENGTH: 866
421 <212> TYPE: PRT
423 <213> ORGANISM: Homo sapiens
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433 Gly Gly Ala Gly Ala Ala Ala Ser Arg Ala Leu Gln Gln Cys Gly Gln
434             20              25              30
437 Leu Gln Lys Leu Ile Asp Ile Ser Ile Gly Ser Leu Arg Gly Leu Arg
438         35              40              45
441 Thr Lys Cys Ala Val Ser Asn Asp Leu Thr Gln Gln Glu Ile Arg Thr
442     50              55              60
445 Leu Glu Ala Lys Leu Val Arg Tyr Ile Cys Lys Gln Arg Gln Cys Lys
446 65              70              75              80
449 Leu Ser Val Ala Pro Gly Glu Arg Thr Pro Glu Leu Asn Ser Tyr Pro
450             85              90              95
453 Arg Phe Ser Asp Trp Leu Tyr Thr Phe Asn Val Arg Pro Glu Val Val
454             100             105             110
457 Gln Glu Ile Pro Arg Asp Leu Thr Leu Asp Ala Leu Leu Glu Met Asn
458         115             120             125
461 Glu Ala Lys Val Lys Glu Thr Leu Arg Arg Cys Gly Ala Ser Gly Asp
462     130             135             140
465 Glu Cys Gly Arg Leu Gln Tyr Ala Leu Thr Cys Leu Arg Lys Val Thr
466 145             150             155             160
469 Gly Leu Gly Gly Glu His Lys Glu Asp Ser Ser Trp Ser Ser Leu Asp
470             165             170             175
473 Ala Arg Arg Glu Ser Gly Ser Gly Pro Ser Thr Asp Thr Leu Ser Ala
474             180             185             190
477 Ala Ser Leu Pro Trp Pro Pro Gly Ser Ser Gln Leu Gly Arg Ala Gly
478         195             200             205
481 Asn Ser Ala Gln Gly Pro Arg Ser Ile Ser Val Ser Ala Leu Pro Ala
482     210             215             220
485 Ser Asp Ser Pro Thr Pro Ser Phe Ser Glu Gly Leu Ser Asp Thr Cys
486 225             230             235             240
489 Ile Pro Leu His Ala Ser Gly Arg Leu Thr Pro Arg Ala Leu His Ser
490             245             250             255
493 Phe Ile Thr Pro Pro Thr Thr Pro Gln Leu Arg Arg His Thr Lys Leu
494             260             265             270
497 Lys Pro Pro Arg Thr Pro Pro Pro Ser Arg Lys Val Phe Gln Leu
498         275             280             285
501 Leu Pro Ser Phe Pro Thr Leu Thr Arg Arg Lys Ser His Glu Ser Gln
502     290             295             300
505 Leu Gly Asn Arg Ile Asp Asp Val Ser Ser Met Arg Phe Asp Leu Ser
506 305             310             315             320
509 His Gly Ser Pro Gln Met Val Arg Arg Asp Ile Gly Leu Ser Val Thr
510             325             330             335
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VERIFICATION SUMMARY
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